>AF249278 ACCESSION:AF249278 NID: gi 9651966 gb AF249278.1 AF249278

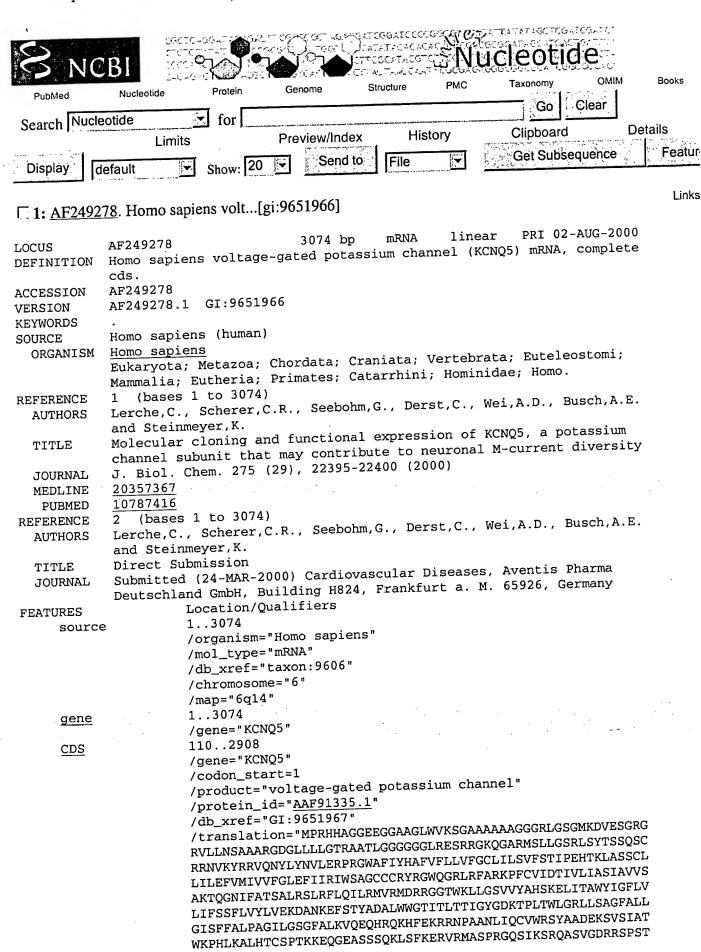
Homo sapiens voltage-gated potassium channel (KCNQ5)

mRNA, complete cds

Length = 3074

Score = 1832 bits (4694), Expect = 0.0 Identities = 920/932 (98%), Positives = 921/932 (98%), Gaps = 9/932 (0%) Frame = +2MPRHHAGGEEGGAAGLWVKSGAAAAAGGGRLGSGMKDVESGRGRVLLNSAAARGDGLLL 60 ${\tt MPRHHAGGEEGGAAGLWVKSGAAAAAAGGGRLGSGMKDVESGRGRVLLNSAAARGDGLLL}$ Query: 1 Sbjct: 110 MPRHHAGGEEGGAAGLWVKSGAAAAAAGGGRLGSGMKDVESGRGRVLLNSAAARGDGLLL 289 LGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRVQNYLYNVLE 120 LGTRAATLGGGGGGLRESRRGKQGARMSLLG LSYTSSQSCRRNVKYRRVQNYLYNVLE Query: 61 Sbjct: 290 LGTRAATLGGGGGGLRESRRGKQGARMSLLGSRLSYTSSQSCRRNVKYRRVQNYLYNVLE 469 RPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEFIIRIW 180 RPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEFIIRIW Query: 121 RPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEFIIRIW 649 Sbjct: 470 Query: 181 SAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLRFLQIL 240 SAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLRFLQIL SAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLRFLQIL 829 Sbjct: 650 RMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEFSTYAD 300 ${\tt RMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEFSTYAD}$ Query: 241 Sbjct: 830 RMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEFSTYAD 1009 ALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQEQHRQ 360 ALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQEQHRQ Query: 301 Sbjct: 1010 ALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQEQHRQ 1189 Query: 361 KHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKPHLKALHTCSPT-----NQKLS 411 KHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKPHLKALHTCSPT Sbjct: 1190 KHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKPHLKALHTCSPTKKEQGEASSSQKLS 1369 Query: 412 FKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLK 471 FKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLK Sbjct: 1370 FKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLK 1549 Query: 472 SSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKET 531 ${\tt SSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKET}$ Sbjct: 1550 SSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKET 1729 Query: 532 LRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEHETTDDL 591 LRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEHETTDDL Sbjct: 1730 LRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEHETTDDL 1909 Query: 592 SMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSP 651 SMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSP Sbjct: 1910 SMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSP 2089 Query: 652 VDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPISQ 711 VDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPISQ Sbjct: 2090 VDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPISQ 2269

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	Query:	712	SDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPNPAGLQESISDV SDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPNPAGLQESISDV SDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPNPAGLQESISDV	771
	Sbjct:	2270		2449
			TTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIRSTE TTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIRSTE TTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIRSTE	
		2450		2027
			ELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETDTFDAAPQPAREAAFAS ELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETDTFDAAPQPAREAAFAS ELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETDTFDAAPQPAREAAFAS	
	Sbjct:	2630		2809
	Query:	892	DSLRTGRSRSSQSICKAGESTDALSLPHVKLK 923 DSLRTGRSRSSQSICKAGESTDALSLPHVKLK DSLRTGRSRSSQSICKAGESTDALSLPHVKLK 2905	
	Sbjct:	2810		



DITAEGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCD VSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKS $\verb|LQTRVDQILGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLL|$ DIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSA NISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAP KPAAPTTLQIPPPLPAIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNL TKDRSMRKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRG ${\tt SQDFYPKWRESKLFITDEEVGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSI}$ CKAGESTDALSLPHVKLK"

BASE COUNT ORIGIN

788 a

784 c

789 g

713 t

.N		h = ==================================	acttectect	tgaaacccgc	cggcgcacat ·	gaggccgctg
241	cagggtgctg	ctgaactcgg	cagecgecag	cctgaggag	agccgccggg	gcaagcaggg
301	cgcggccacg	cttggtggcg	geggeggegg	cctgagggag	agtagccaga	gctgccggcg
961	ctatctggtg	gaaaaggatg	ccaataaaga	gttttctaca	actoccotaa	cttaactaaa
1021	gggcacaatt	acattgacaa	ctattggcta	tggagacaaa	ttatttacac	ttactaccaa
1081	aagattgctt	tctgcaggct	ttgcactcct	tggcatttct	caccaccaca	aacactttga
1141	cattcttggc	tcaggttttg	cattaaaagt	acaagaacaa	taccateatt	acacaactaa
2222	gettageee	accaccaaca	ccattgcaaa	a ccaaataaat	acggcaccca	agccagcagc ccaggccaga
234.	L cccaccaci	cotaecct	caggettaca	a ggaaagcatt	: tctgacgtca	ccacctgcct accgttctat
240.	l aactetgea	- cogganaat	ttcaggttg	acagtcaaat	ctcaccaagg	accgttctat tggtgccgaa
246	l tgttgcctco	c aayyaaaac	ascusation of	tctattatct	gtctgtccca	tggtgccgaa aactgaatat
252	1 gaggaaaag	c titgacaty	y gaggagaaa.	cctgatcagg	tcgaccgagg	aactgaatat accccaaatg
258	l ggacttggg	c addicting	t caadtaact	cagaggcag	caagatttt	accccaaatg a cagagacaga
264	1 acaactttc	a gggagtgag	taagtyget	a agaggtaggt	cccgaagaga	a cagagacaga g actctctaag
270	1 gagggaatc	c aaattgttt	a laactyaty	a agaaactac	tttgcatcag	actctctaag a cagatgccct
276	1 cacttttga	t gccgcaccg	e agectigeea	t ttataaaac	ngagaagta	a cagatgccct
282	1 gactggaag	g tcacgatca	- tannatana	t tottoatiti	t ctttccagg	atagcagttc
288	1 cagcttgcc	t catgtcaaa	c iyaaataay		, ,	

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2941 tttagccata catatcattg catgaactat ttcgaaagcc cttctaaaaa gttgaaattg 3001 caagaatcgg gaagaacatg aaaggcagtt tataagcccg ttacctttta attgcatgaa 3061 aatgcatgtt tagg

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Oct 1 2003 15:02:47